

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 12:30:13 ; Search time 92 seconds
(without alignments)
4.479 Million cell updates/sec

Title: SHORT-PEP
Perfect score: 16
Sequence: 1 rw 2

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 4
Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacteriap:*
17: SP-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	37.5	5	P83308	P83308 gallus galli
2	2	12.5	4	11 Q08433	Q08433 rattus norv
3	2	12.5	5	2 P83073	P83073 bacillus ce
4	2	12.5	5	10 Q99007	Q99007 hordeum vul

ALIGNMENTS

RESULT 1
ID P83308 PRELIMINARY; PRT; 5 AA.
AC P83308;
DT 01-JUN-2002 (TREMREL. 21, Created)
DT 01-JUN-2002 (TREMREL. 21, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)

DE FMRFamide-like neuropeptide (FLRF-amide).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-BRAIN;
RX PubMed=6137771;
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
antibodies to FMRFamide."
RL Nature 305:328-330(1983).
CC -1- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 37.5%; Score 6; DB 13; Length 5;
Best Local Similarity 50.0%; Pred. NO. 6.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RW 2
DB 4 RF 5

RESULT 2
ID Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 01-JAN-1999 (TREMREL. 09, Last annotation update)
DE UDP-glucuronosyltransferase, microsomal (EC 2.4.1.17) (UDPGT)
DE (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GUNN;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Kolwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROsome.
DR EMBL: S38636; AAB19259.1;
KW Transferase; glycosyltransferase; Microsome; Multigene family.
FT NON-TER 1 1
FT NON-TER 4 4
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 12.5%; Score 2; DB 11; Length 4;
Best Local Similarity 0.0%; Pred. NO. 6.7e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 R 1
DB 4 K 4
RESULT 3
P83073

ID P83073 PRELIMINARY; PRT; 5 AA.
 AC P83073;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE 88 kDa protein (Fragment).
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN 11
 RP SEQUENCE.
 RC STRAIN=NCIMB 11796;
 RA Browne N., Dowds B.C.A.;
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.
 FT NON_TER 5
 SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 12.5%; Score 2; DB 2; Length 5;
 Best Local Similarity 0.0%; Pred. No. 6.7e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
 Db 2 K 2

RESULT 4

Q99007 PRELIMINARY; PRT; 5 AA.
 AC Q99007;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE Alpha-amylase (EC 3.2.1.1) (Fragment).
 GN AMY1.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
 RX MEDLINE=91329704; PubMed=1831055;
 RA Jacobsen J.V., Close T.J.;
 RT "Control of transient expression of chimeric genes by gibberellic
 RT acid and abscisic acid in protoplasts prepared from mature barley
 RT aleurone layers".
 RL Plant Mol. Biol. 16:713-721(1991).
 CC -1- CATALYTIC ACTIVITY: ENDOMYDOLYSIS OF 1,4-ALPHA-GLUCOSIDIC
 CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
 CC BARLEY.
 DR EMBL; X54643; CAA38455.1; -
 KW Hydrolase; Glycosylase; Carbohydrate metabolism; Seed; Germination;
 FT NON_TER 5
 SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 12.5%; Score 2; DB 10; Length 5;
 Best Local Similarity 0.0%; Pred. No. 6.7e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
 Db 4 K 4

Search completed: February 21, 2003, 12:33:48
 Job time : 93 secs